

SEQUENCE LISTING

<110> Jing, Shuqian

<120> Transforming Growth Factor-Beta-Related Molecules and
Uses Thereof

<130> 00-659-A

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<150> 60/253,476

<151> 2000-11-28

<160> 27

<170> PatentIn Ver. 2.0

<210> 1

<211> 665

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (80)..(502)

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Met Val Leu Pro Ser Tyr Ser Lys Lys Pro Leu
1 5 10

atc tct aat gtg gag cag ctg atc ctg ggg atc ccg ggc cag aat cgc 160
Ile Ser Asn Val Glu Gln Leu Ile Leu Gly Ile Pro Gly Gln Asn Arg
15 20 25

cgg gag ata ggc cat ggc cag gat atc ttt cca gca gag aag ctc tgc 208
Arg Glu Ile Gly His Gly Gln Asp Ile Phe Pro Ala Glu Lys Leu Cys
30 35 40

cat ctg cag gat cgc aag gtg aac ctt cac aga gct gcc tgg ggc gag 256
His Leu Gln Asp Arg Lys Val Asn Leu His Arg Ala Ala Trp Gly Glu
45 50 55

tgt att gtt gca ccc aag act ctc agc ttc tct tac tgt cag ggg acc 304
Cys Ile Val Ala Pro Lys Thr Leu Ser Phe Ser Tyr Cys Gln Gly Thr
60 65 70 75

tgc ccg gcc ctc aac agt gag ctc cgt cat tcc agc ttt gag tgc tat 352
Cys Pro Ala Leu Asn Ser Glu Leu Arg His Ser Ser Phe Glu Cys Tyr
80 85 90

aag agg gca gta cct acc tgt ccc tgg ctc ttc cag acc tgc cgt ccc 400
Lys Arg Ala Val Pro Thr Cys Pro Trp Leu Phe Gln Thr Cys Arg Pro

95

100

105

acc atg gtc aga ctc ttc tcc ctg atg gtc cag gat gac gaa cac aag 448
 Thr Met Val Arg Leu Phe Ser Leu Met Val Gln Asp Asp Glu His Lys
 110 115 120

atg agt gtg cac tat gtg aac act tcc ttg gtg gag aag tgt ggc tgc 496
 Met Ser Val His Tyr Val Asn Thr Ser Leu Val Glu Lys Cys Gly Cys
 125 130 135

tct tga gatacccaa agcctcctac tggcctcagg gccacctaag tctcaggact 552
 Ser
 140

tttagtagggg gtgggattac ttttcatagc aagtagagct ctttgaaggg aggtgggatt 612

tggtttgttt ctcaaagcac agcaagaagg ttggcattat ggcagtaaca aat 665

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 <212> PRT
 <213> Homo sapiens

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Gly Gln Asp Ile Phe Pro Ala Glu Lys Leu Cys His Leu Gln Asp Arg
 35 40 45

Lys Val Asn Leu His Arg Ala Ala Trp Gly Glu Cys Ile Val Ala Pro
 50 55 60

Lys Thr Leu Ser Phe Ser Tyr Cys Gln Gly Thr Cys Pro Ala Leu Asn
 65 70 75 80

Ser Glu Leu Arg His Ser Ser Phe Glu Cys Tyr Lys Arg Ala Val Pro
 85 90 95

Thr Cys Pro Trp Leu Phe Gln Thr Cys Arg Pro Thr Met Val Arg Leu
 100 105 110

Phe Ser Leu Met Val Gln Asp Asp Glu His Lys Met Ser Val His Tyr
 115 120 125

Val Asn Thr Ser Leu Val Glu Lys Cys Gly Cys Ser
 130 135 140

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 <213> Homo sapiens

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<222> (61)..(648)

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atg aga ttt ttt tct gcc agg caa cat ggt ttt acc ctc ata ttc aaa 108
Met Arg Phe Phe Ser Ala Arg Gln His Gly Phe Thr Leu Ile Phe Lys
1 5 10 15
aag aca aag att cca gcc act gat gtc gct gat gcc agc ctg aat gaa 156
Lys Thr Lys Ile Pro Ala Thr Asp Val Ala Asp Ala Ser Leu Asn Glu
20 25 30
tgt tcc agt acc gaa agg aaa caa gac gta gtg ttg ctg ttc gtg acc 204
Cys Ser Ser Thr Glu Arg Lys Gln Asp Val Val Leu Leu Phe Val Thr
35 40 45
ttg tcc cac aca cag cca cct ctg ttt cac ctg cct tat gtc cag aaa 252
Leu Ser His Thr Gln Pro Pro Leu Phe His Leu Pro Tyr Val Gln Lys
50 55 60
ccc tta atc tct aat gtg gag cag ctg atc ctg ggg atc ccg ggc cag 300
Pro Leu Ile Ser Asn Val Glu Gln Leu Ile Leu Gly Ile Pro Gly Gln
65 70 75 80
aat cgc cgg gag ata ggc cat ggc cag gat atc ttt cca gca gag aag 348
Asn Arg Arg Glu Ile Gly His Gln Asp Ile Phe Pro Ala Glu Lys
85 90 95
ctc tgc cat ctg cag gat cgc aag gtg aac ctt cac aga gct gcc tgg 396
Leu Cys His Leu Gln Asp Arg Lys Val Asn Leu His Arg Ala Ala Trp
100 105 110
ggc gag tgt att gtt gca ccc aag act ctc agc ttc tct tac tgt cag 444
Gly Glu Cys Ile Val Ala Pro Lys Thr Leu Ser Phe Ser Tyr Cys Gln
115 120 125
ggg acc tgc ccg gcc ctc aac agt gag ctc cgt cat tcc agc ttt gag 492
Gly Thr Cys Pro Ala Leu Asn Ser Glu Leu Arg His Ser Ser Phe Glu
130 135 140
tgc tat aag agg gca gta cct acc tgt ccc tgg ctc ttc cag acc tgc 540
Cys Tyr Lys Arg Ala Val Pro Thr Cys Pro Trp Leu Phe Gln Thr Cys
145 150 155 160
cgt ccc acc atg gtc aga ctc ttc tcc ctg atg gtc cag gat gac gaa 588
Arg Pro Thr Met Val Arg Leu Phe Ser Leu Met Val Gln Asp Asp Glu
165 170 175
cac aag atg agt gtg cac tat gtg aac act tcc ttg gtg gag aag tgt 636
His Lys Met Ser Val His Tyr Val Asn Thr Ser Leu Val Glu Lys Cys
180 185 190
ggc tgc tct tga gatacccaa agcctcctac tggcctcagg gccacctaag 688

Gly Cys Ser
195

tctcaggact ttagtagggg gtgggattac ttttcatagc aagtagagct ctttgaaggg 748

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tc 810

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20 25 30

Cys Ser Ser Thr Glu Arg Lys Gln Asp Val Val Leu Leu Phe Val Thr
35 40 45

Leu Ser His Thr Gln Pro Pro Leu Phe His Leu Pro Tyr Val Gln Lys
50 55 60

Pro Leu Ile Ser Asn Val Glu Gln Leu Ile Leu Gly Ile Pro Gly Gln
65 70 75 80

Asn Arg Arg Glu Ile Gly His Gly Gln Asp Ile Phe Pro Ala Glu Lys
85 90 95

Leu Cys His Leu Gln Asp Arg Lys Val Asn Leu His Arg Ala Ala Trp
100 105 110

Gly Glu Cys Ile Val Ala Pro Lys Thr Leu Ser Phe Ser Tyr Cys Gln
115 120 125

Gly Thr Cys Pro Ala Leu Asn Ser Glu Leu Arg His Ser Ser Phe Glu
130 135 140

Cys Tyr Lys Arg Ala Val Pro Thr Cys Pro Trp Leu Phe Gln Thr Cys
145 150 155 160

Arg Pro Thr Met Val Arg Leu Phe Ser Leu Met Val Gln Asp Asp Glu
165 170 175

His Lys Met Ser Val His Tyr Val Asn Thr Ser Leu Val Glu Lys Cys
180 185 190

Gly Cys Ser
195

<210> 5

<211> 214
<212> PRT
<213> Mus musculus

<400> 5
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Phe Val Leu Arg Ser Val Pro Trp Pro Gln Gly Ala Val His Phe Asn
20 25 30
Leu Leu Asp Val Ala Lys Asp Trp Asn Asp Asn Pro Arg Lys Asn Phe
35 40 45
Gly Leu Phe Leu Glu Ile Leu Val Lys Glu Asp Arg Asp Ser Gly Val
50 55 60
Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg Leu Arg Cys Ser Leu His
65 70 75 80
Ala Ser Leu Leu Val Val Thr Leu Asn Pro Asp Gln Cys His Pro Ser
85 90 95
Arg Lys Arg Arg Ala Ala Ile Pro Val Pro Lys Leu Ser Cys Lys Asn
100 105 110
Leu Cys His Arg His Gln Leu Phe Ile Asn Phe Arg Asp Leu Gly Trp
115 120 125
His Lys Trp Ile Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His
130 135 140
Gly Glu Cys Pro Phe Ser Leu Thr Ile Ser Leu Asn Ser Ser Asn Tyr
145 150 155 160
Ala Phe Met Gln Ala Leu Met His Ala Val Asp Pro Glu Ile Pro Gln
165 170 175
Ala Val Cys Ile Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln
180 185 190
Asp Asn Asn Asp Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val
195 200 205
Asp Glu Cys Gly Cys Gly
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<212> DNA
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<222> (380)..(403)
<223> coding portion of exon 1

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<222> (1420)..(1671)
<223> exon 2

<220>
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<222> (2024)..(2170)
<223> coding portion of exon 3

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gatcagctac aagctgtggg gggtagaat agggctaca gctgggcacg tggatattta 180
aagacagcga aggggaagcc ccgcctctga gaggatgtat gttggagggt ggctgtggga 240
gaagtggcag ctccctggctc attcctgggc tcttggctct gggctttgg tgcattgttt 300
tgagctcagt agagacgttt gactgtccca acccgatgt gccttccac ataaatgaga 360
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<212> PRT
<213> Homo sapiens

<400> 7
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<210> 8
<211> 84
<212> PRT
<213> Homo sapiens

<400> 8
Lys Pro Leu Ile Ser Asn Val Glu Gln Leu Ile Leu Gly Ile Pro Gly
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Gln Asn Arg Arg Glu Ile Gly His Gly Gln Asp Ile Phe Pro Ala Glu
20 25 30

Lys Leu Cys His Leu Gln Asp Arg Lys Val Asn Leu His Arg Ala Ala
35 40 45

Trp Gly Glu Cys Ile Val Ala Pro Lys Thr Leu Ser Phe Ser Tyr Cys
50 55 60

Gln Gly Thr Cys Pro Ala Leu Asn Ser Glu Leu Arg His Ser Ser Phe
65 70 75 80

Glu Cys Tyr Lys

<210> 9
<211> 48
<212> PRT
<213> Homo sapiens

<400> 9
Arg Ala Val Pro Thr Cys Pro Trp Leu Phe Gln Thr Cys Arg Pro Thr
1 5 10 15

Met Val Arg Leu Phe Ser Leu Met Val Gln Asp Asp Glu His Lys Met
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Ser Val His Tyr Val Asn Thr Ser Leu Val Glu Lys Cys Gly Cys Ser
35 40 45

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<211> 2940
<212> DNA
<213> Homo sapiens

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<222> (355)..(402)
<223> coding portion of exon 1

<220>
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<222> (1282)..(1671)
<223> exon 2

<220>
<221> exon
<222> (2024)..(2170)
<223> coding portion of exon 3

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tgagctcagt agagacgttt gactgtccca acccgatgct gccttccac ataa atg 357
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cct ctg ttt cac ctg cct tat gtc cag aaa ccc tta atc tct aat gtg 1440
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cat ggc cag gat atc ttt cca gca gag aag ctc tgc cat ctg cag gat 1536
cgc aag gtg aac ctt cac aga gct gcc tgg ggc gag tgt att gtt gca 1584
ccc aag act ctc agc ttc tct tac tgt cag ggg acc tgc ccg gcc ctc 1632
aac agt gag ctc cgt cat tcc agc ttt gag tgc tat aag gtaagacatg 1681
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<213> Homo sapiens

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1 5 10 15

<210> 12
<211> 131
<212> PRT
<213> Homo sapiens

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1 5 10 15

Cys Ser Ser Thr Glu Arg Lys Gln Asp Val Val Leu Leu Phe Val Thr
20 25 30

Leu Ser His Thr Gln Pro Pro Leu Phe His Leu Pro Tyr Val Gln Lys
35 40 45

Pro Leu Ile Ser Asn Val Glu Gln Leu Ile Leu Gly Ile Pro Gly Gln
50 55 60

Asn Arg Arg Glu Ile Gly His Gln Asp Ile Phe Pro Ala Glu Lys
65 70 75 80

Leu Cys His Leu Gln Asp Arg Lys Val Asn Leu His Arg Ala Ala Trp
85 90 95

Gly Glu Cys Ile Val Ala Pro Lys Thr Leu Ser Phe Ser Tyr Cys Gln
100 105 110

Gly Thr Cys Pro Ala Leu Asn Ser Glu Leu Arg His Ser Ser Phe Glu
115 120 125

Cys Tyr Lys
130

<210> 13
<211> 48
<212> PRT
<213> Homo sapiens

<400> 13
Arg Ala Val Pro Thr Cys Pro Trp Leu Phe Gln Thr Cys Arg Pro Thr

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Met Val Arg Leu Phe Ser Leu Met Val Gln Asp Asp Glu His Lys Met
20 25 30

Ser Val His Tyr Val Asn Thr Ser Leu Val Glu Lys Cys Gly Cys Ser
35 40 45

<210> 14

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<212> PRT

<213> Human immunodeficiency virus type 1

<400> 14

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 15

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: internalizing
domain derived from HIV tat protein

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1 5 10 15

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR primer
2445-27

<400> 16

ctcatattca aatatcagagg gaggg 25

<210> 17

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
2445-28

<400> 17

gtttactcac gtattggatg gaggtg 26

<210> 18
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer
2445-29

<400> 18
ctctaatgtg gagcagctga tc

22

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
2450-21

<400> 19
cagcagagaa gctctgccat ctgc

24

<210> 20
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer
2445-30

<400> 20
gagcagccac acgggttctc caccaag

27

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
2445-31

<400> 21
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24

<210> 22
<211> 23
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
2445-32

<400> 22
ctcatcttgt gttcgtcatac ctg 23

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
2445-22

<400> 23
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<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RACE primer
1916-83

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: RACE primer
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<211> 29

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<213> Artificial Sequence

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1916-81

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